

00000000000000000000000000000000

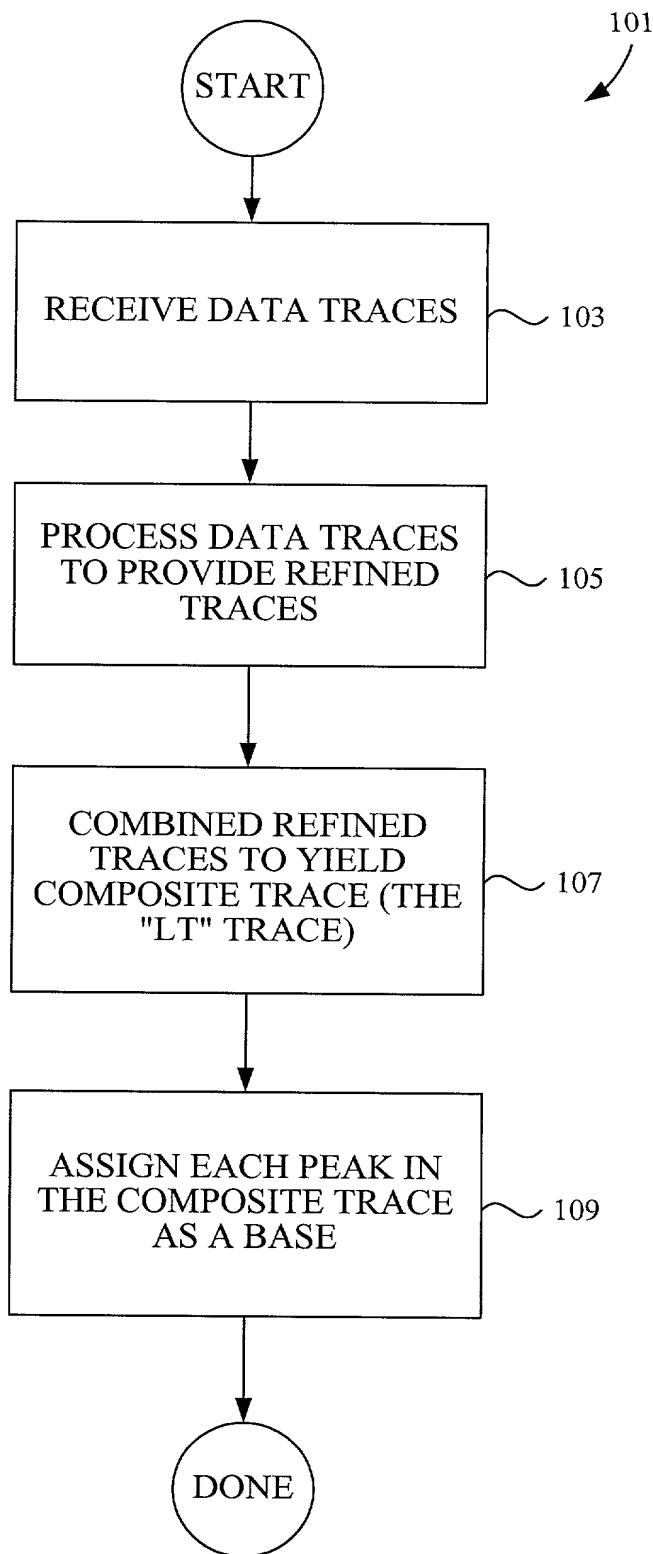


FIG. 1

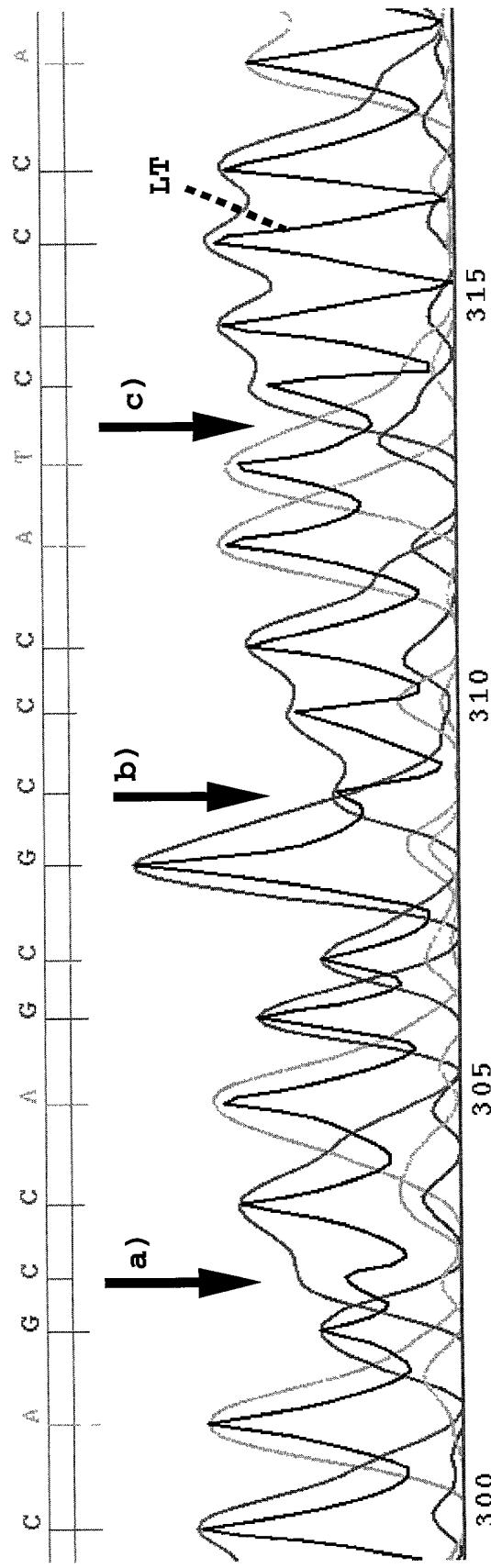


FIG. 2

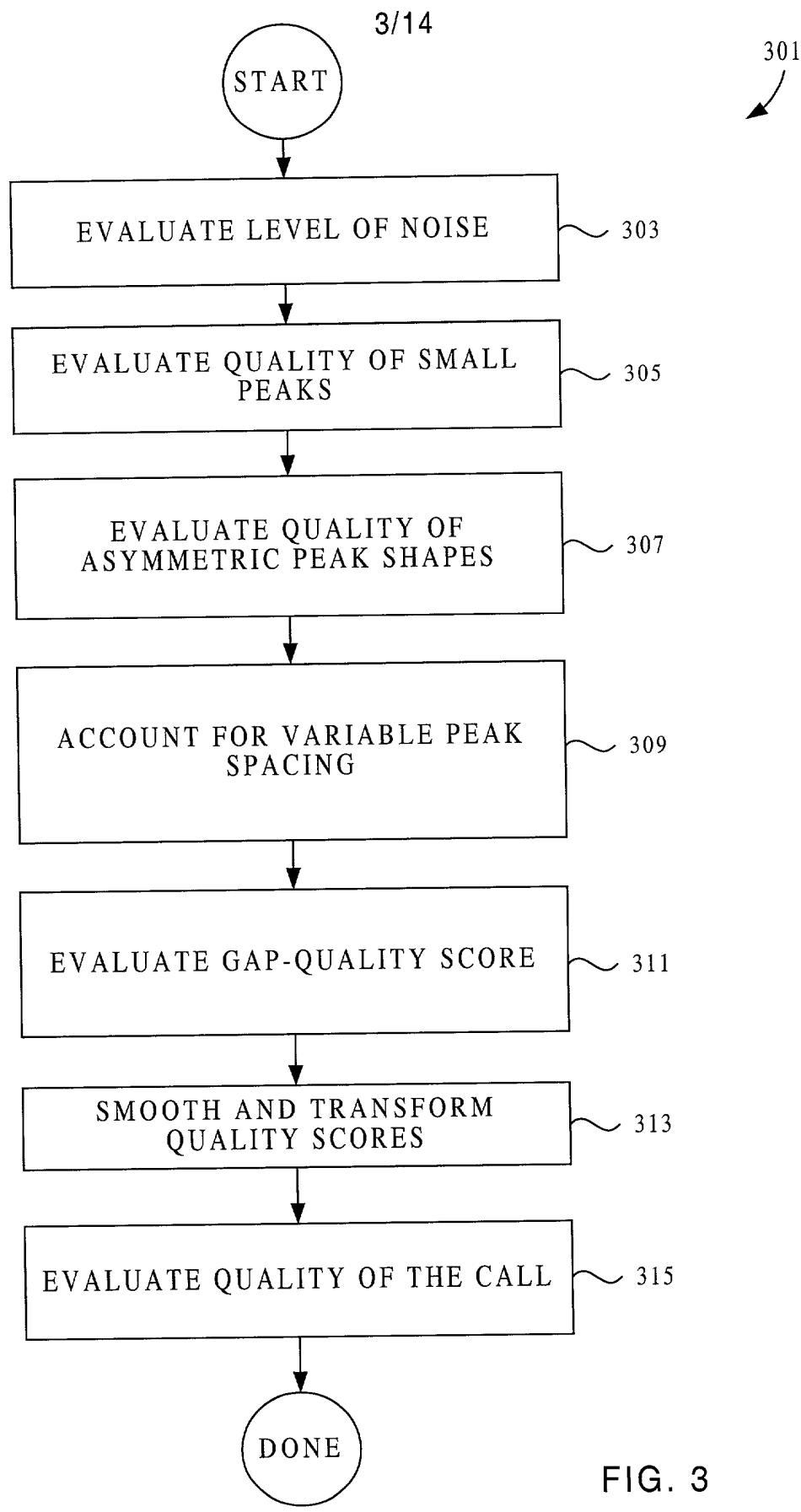
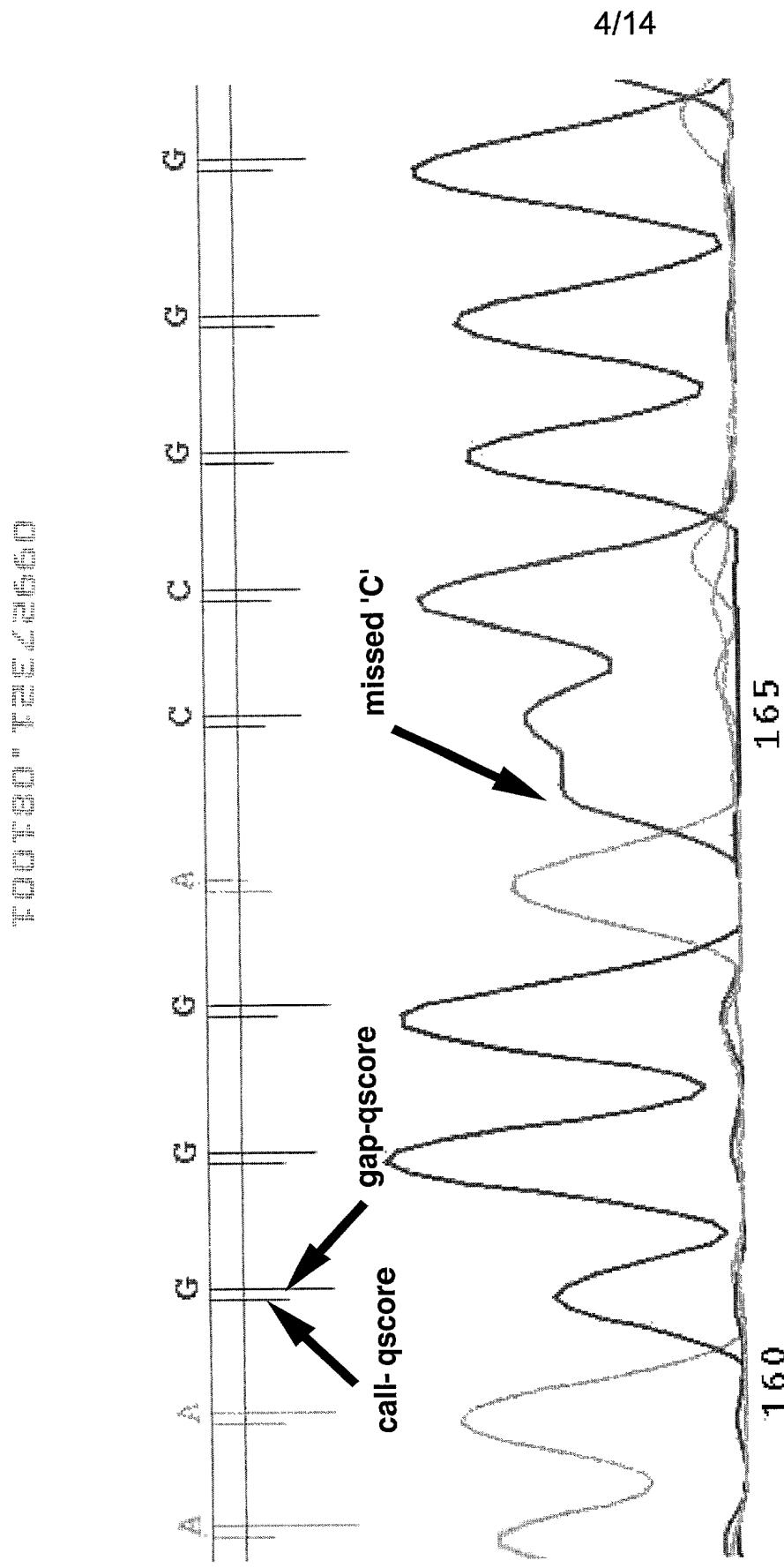


FIG. 3



AAGGGACCCGGG true sequence

alignment alternatives:

AACGGACC-GGG

AACGGAC-CGGG

AACGGAA-CCGGG correct alignment

FIG. 4

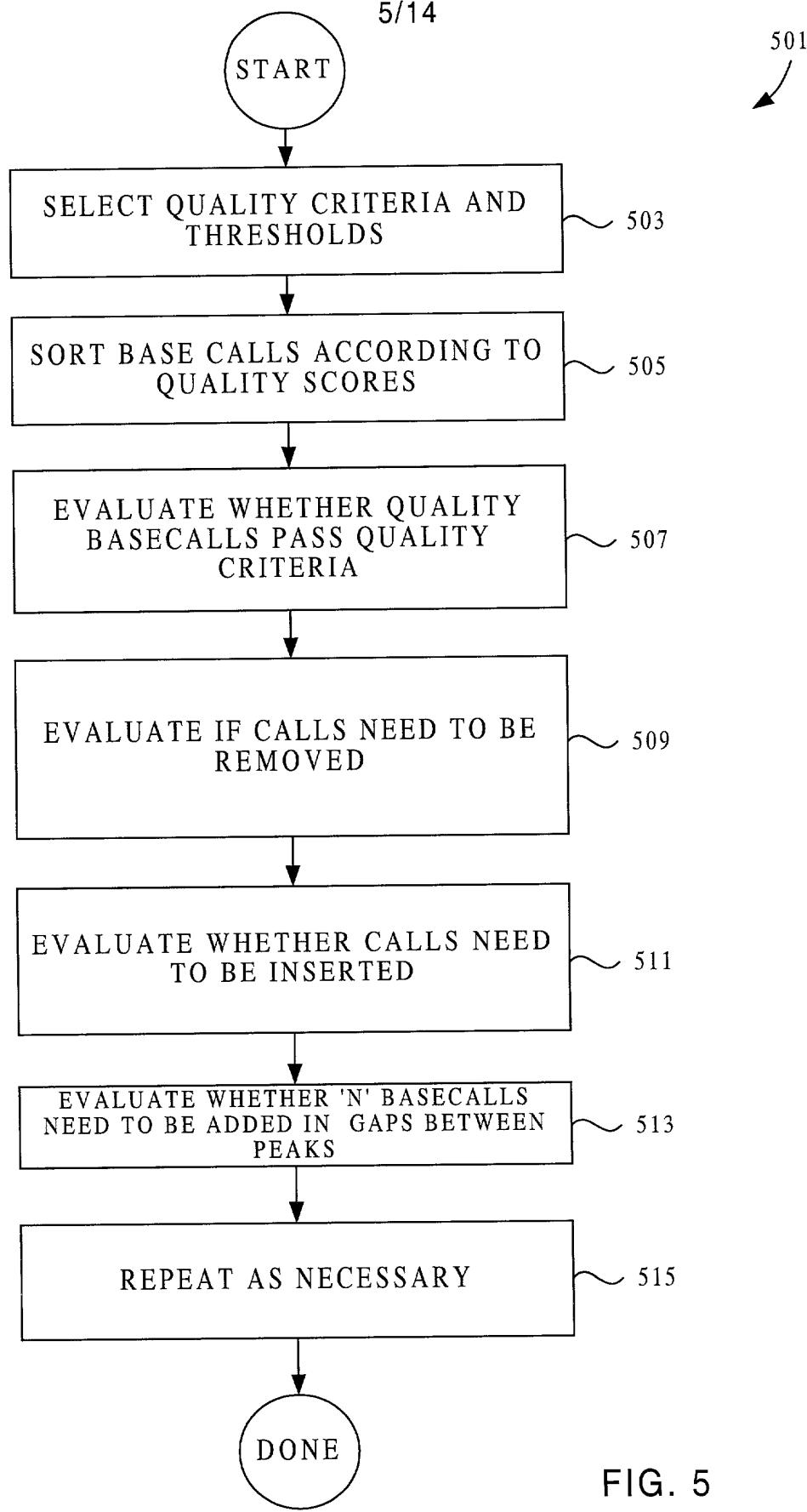


FIG. 5

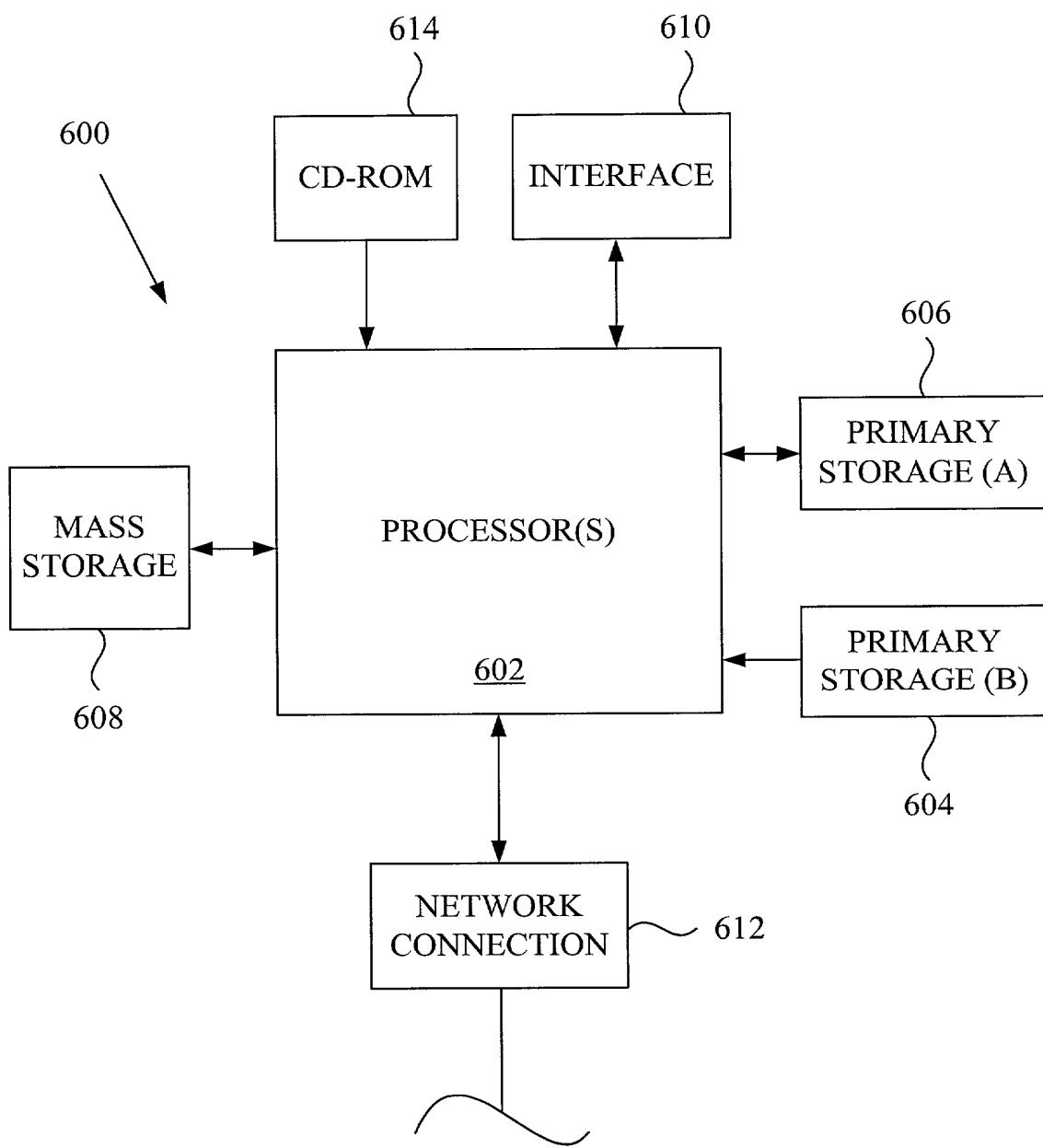
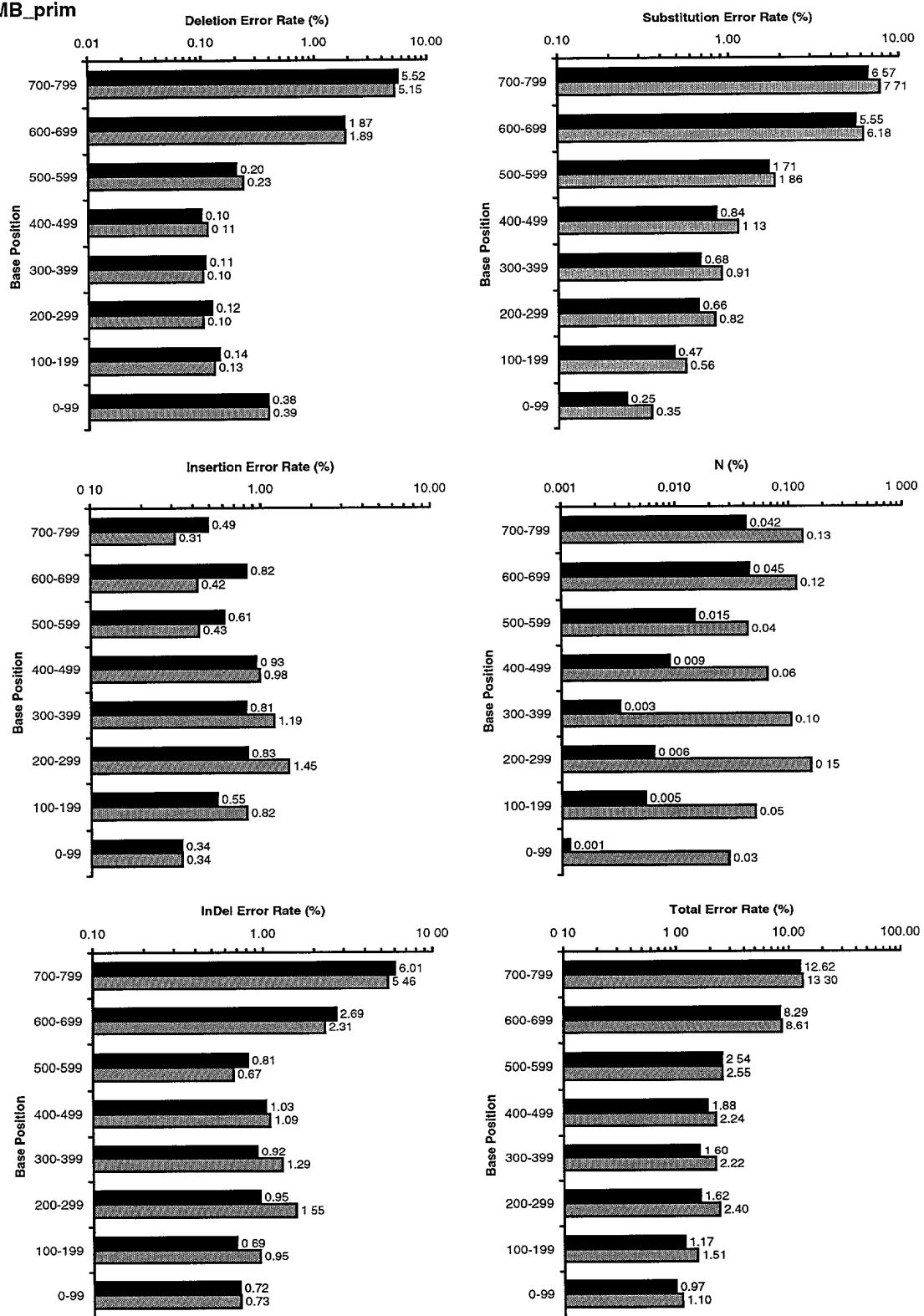


FIG. 6

MB_prim**FIG. 7A**

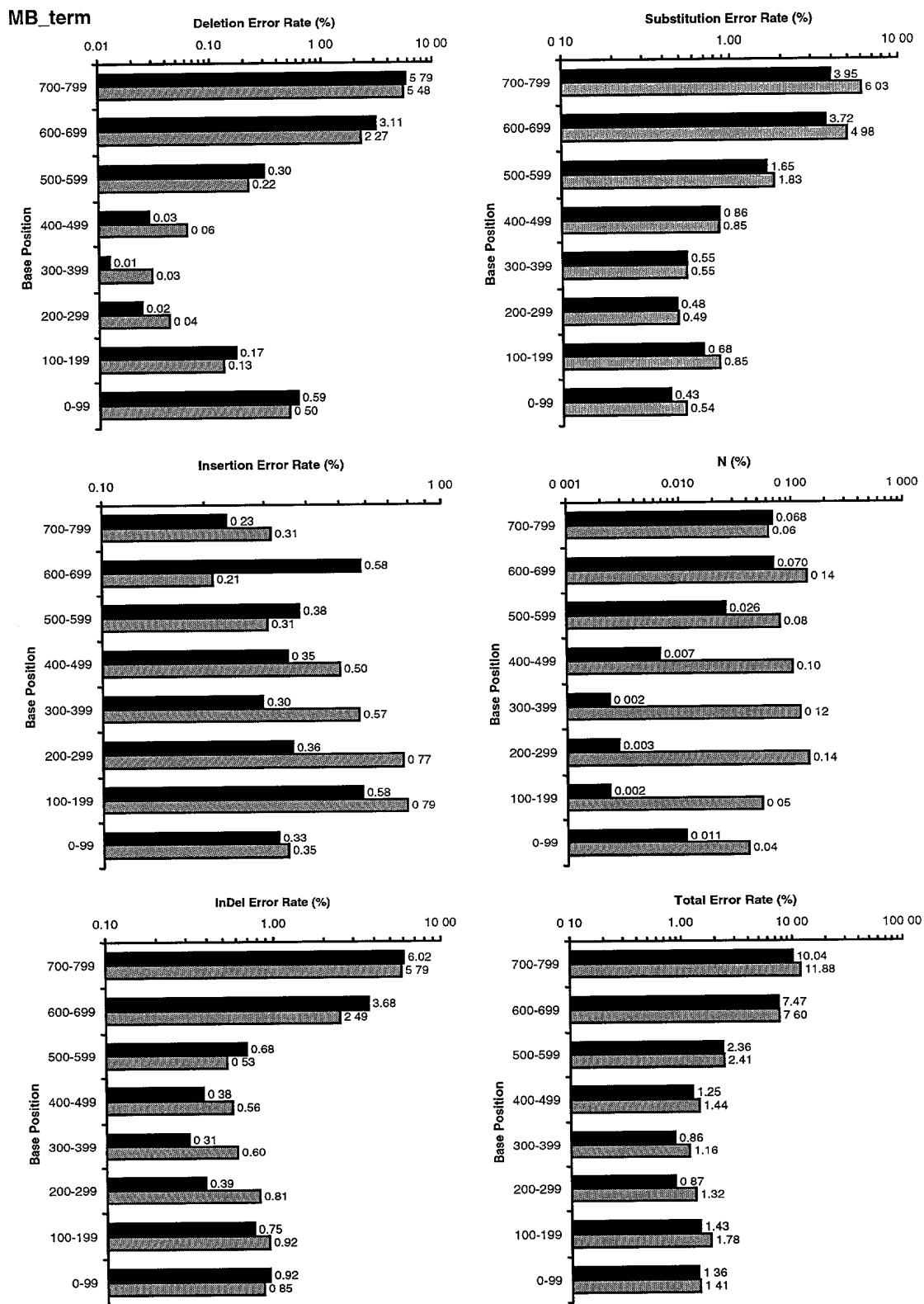


FIG. 7B

9/14

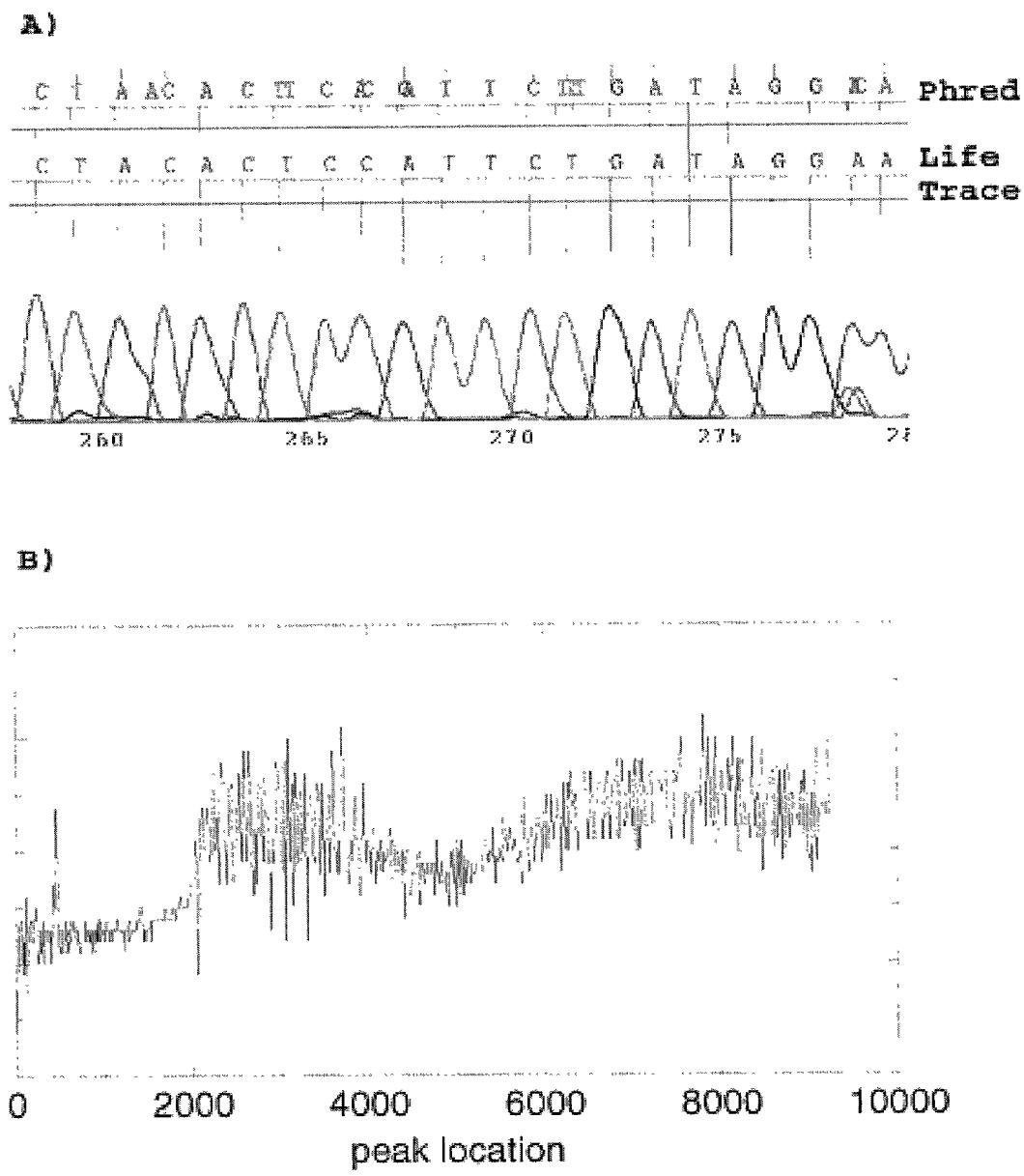
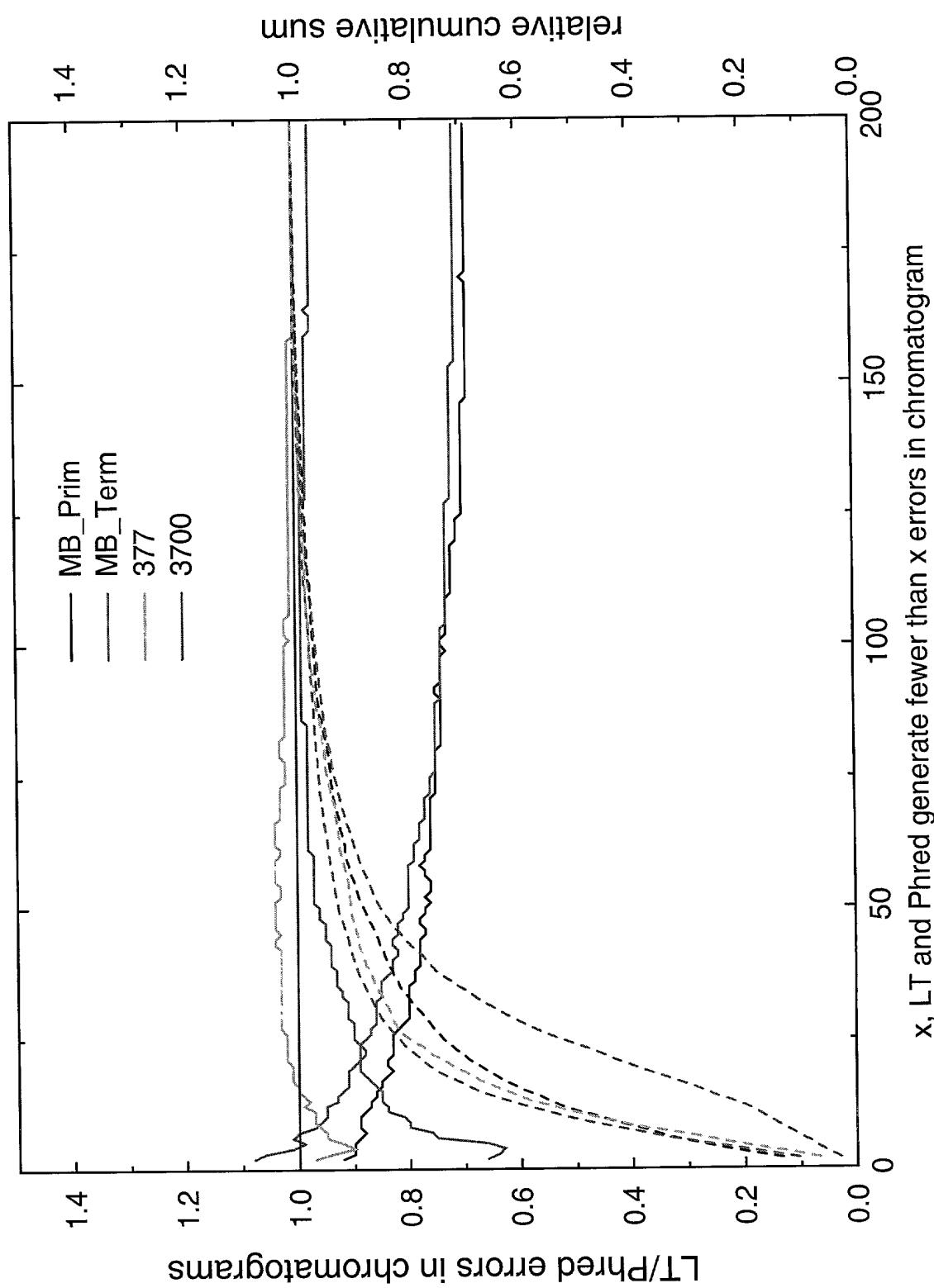


FIG. 8



X, LT and Phred generate fewer than x errors in chromatogram

FIG. 9

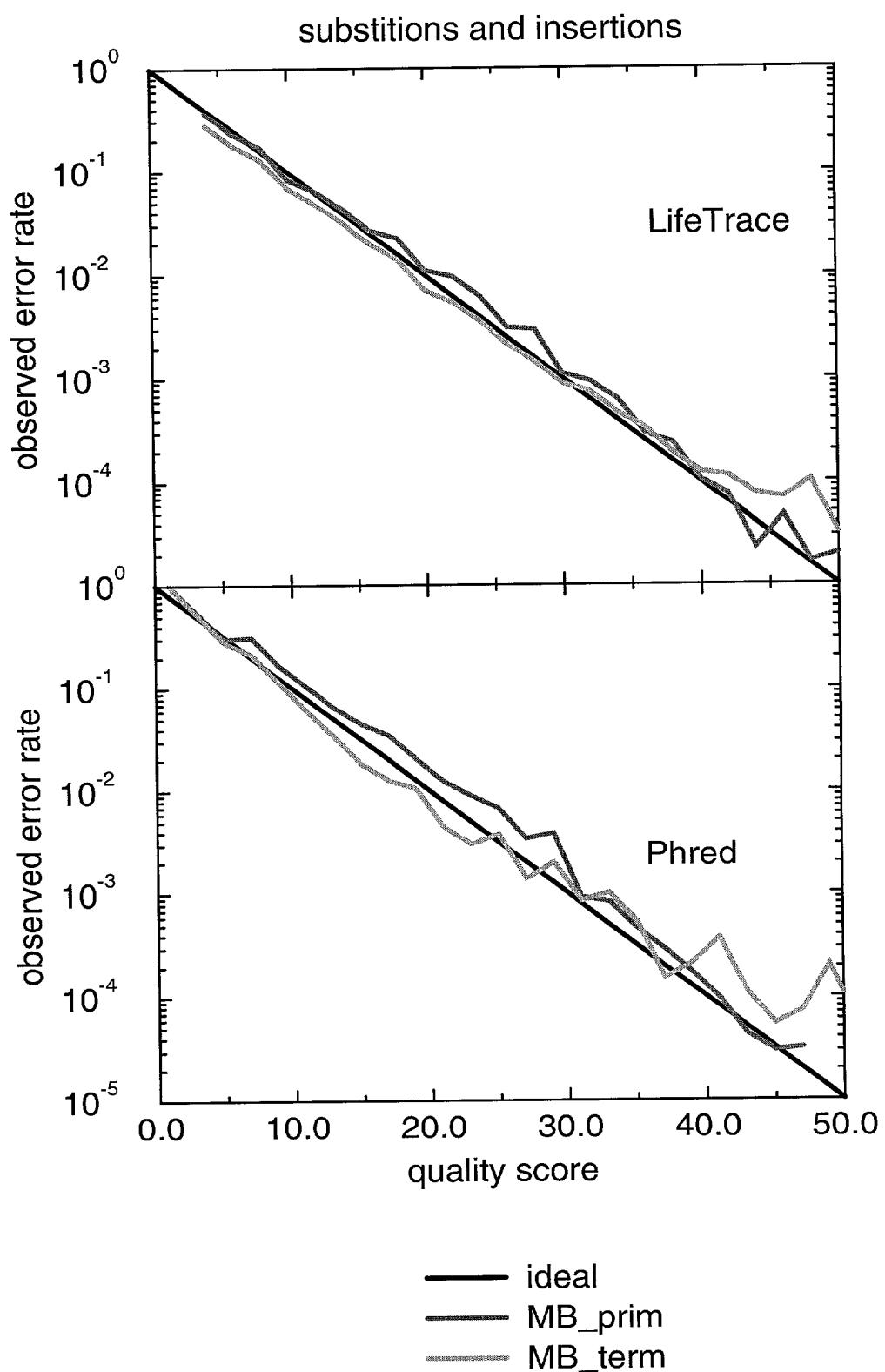


FIG. 10

12/14

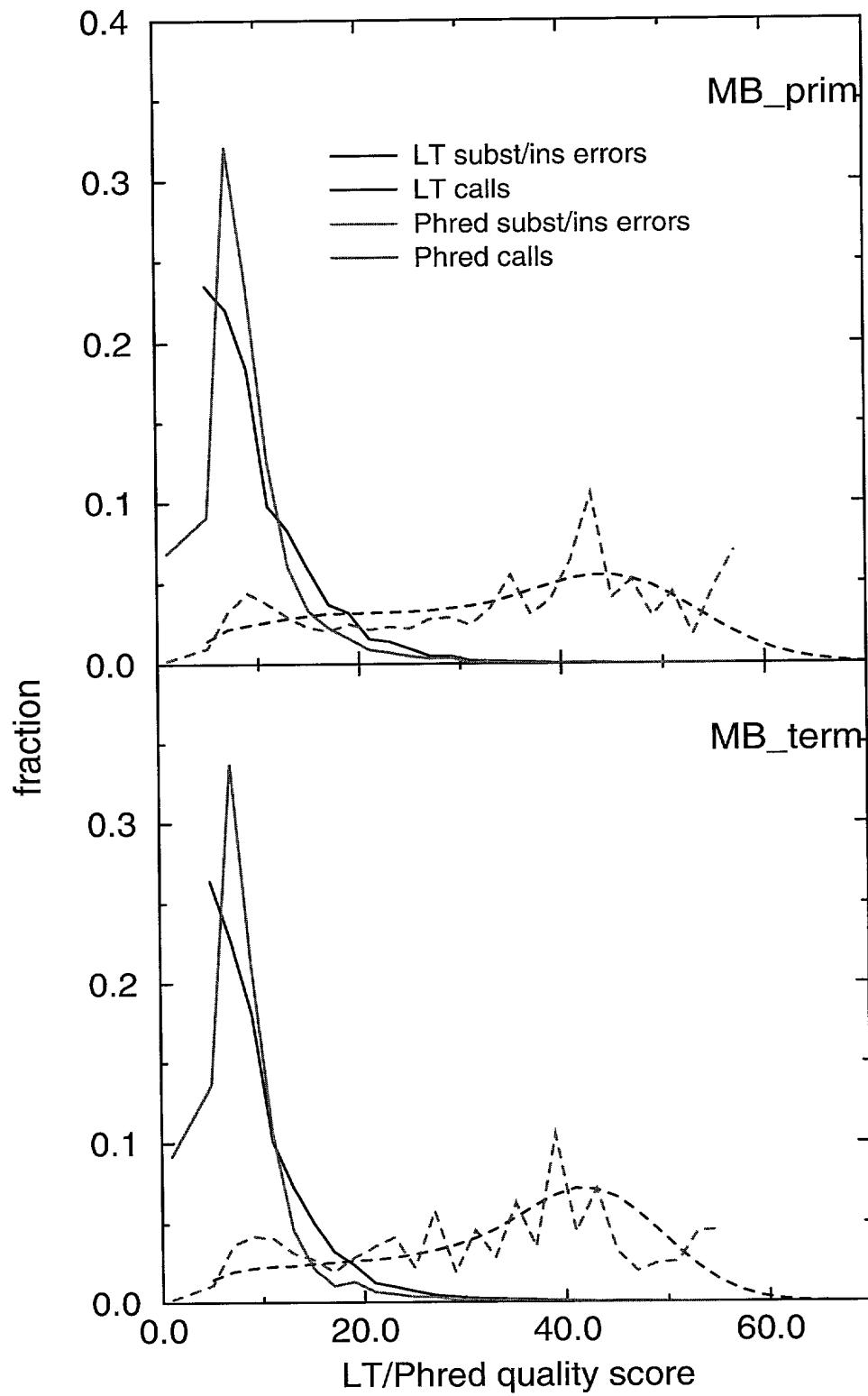


FIG. 11

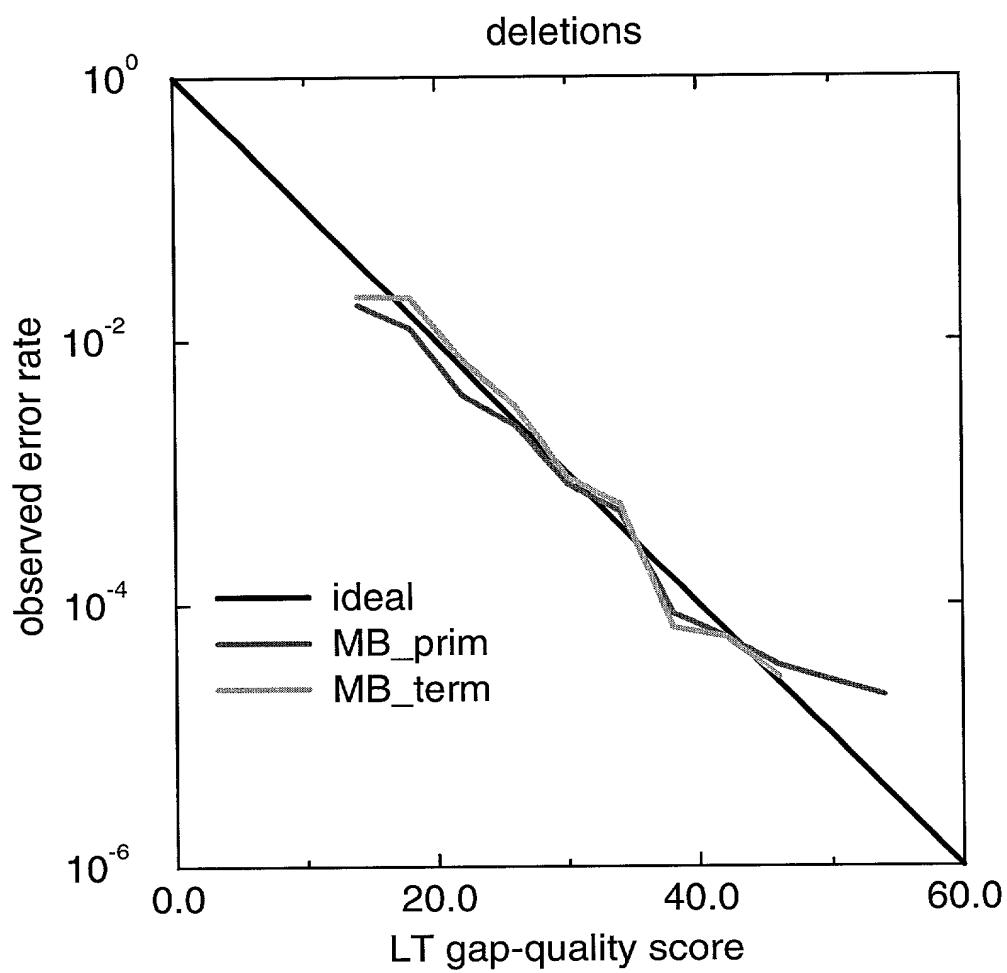


FIG. 12

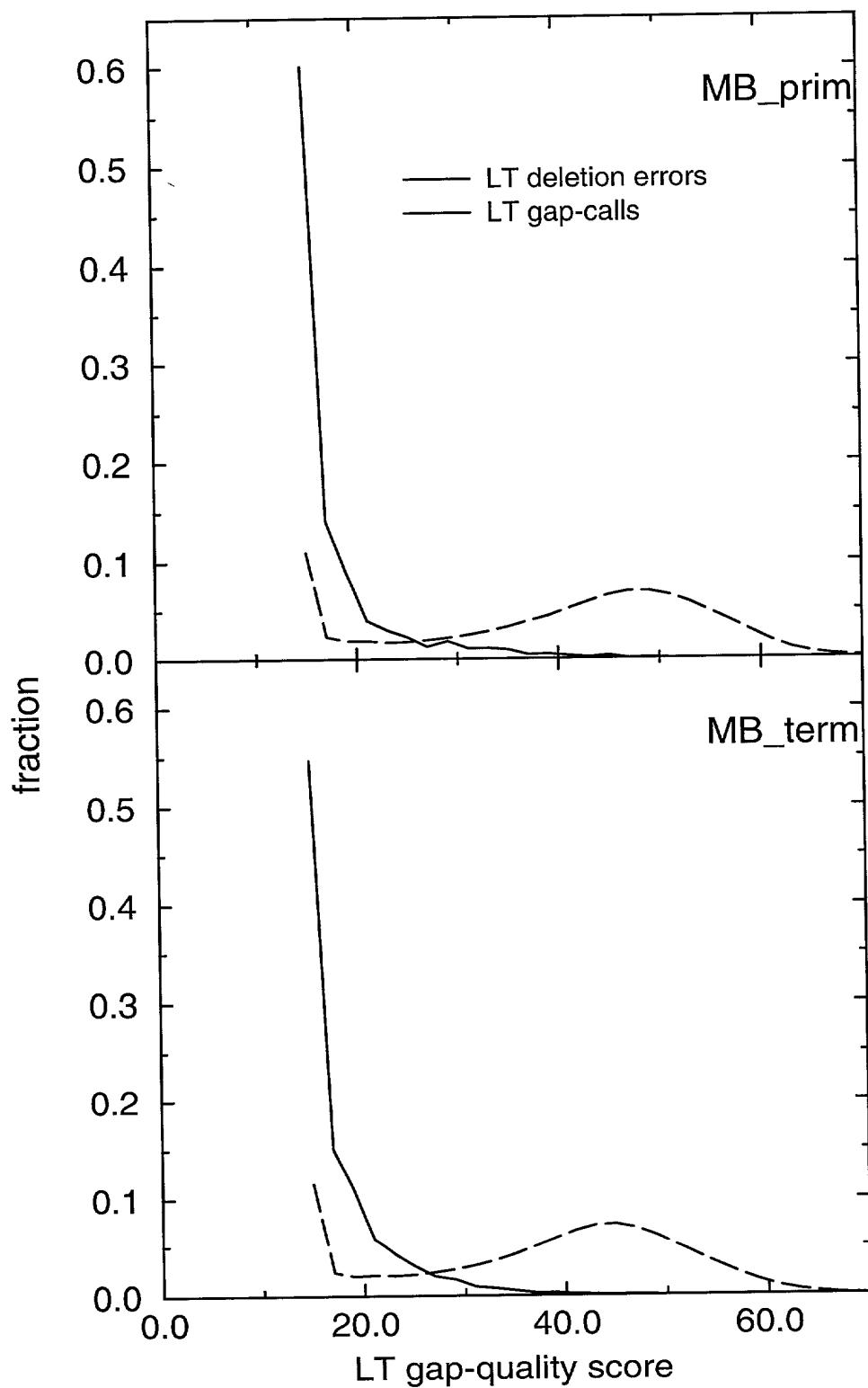


FIG. 13